

JUN 21 2001

TECH CENTER 1600/2900

DATE: 05/21/2001  
TIME: 11:18:381600 #  
14  
ENTEREDRAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/369,735AInput Set : A:\11059 002001.TXT  
Output Set: N:\CRF3\05212001\I369735A.raw

4 <110> APPLICANT: Matsui, Ikuo  
5 Ishikawa, Kazuhiko  
6 Ishida, Hiroyasu  
7 Kosugi, Yoshitsugu  
9 <120> TITLE OF INVENTION: THERMOPHILIC ENZYMES HAVING  
10 BETA-GLYCOSIDASE ACTIVITY  
12 <130> FILE REFERENCE: 11059/002001  
14 <140> CURRENT APPLICATION NUMBER: 09/369,735A  
15 <141> CURRENT FILING DATE: 1999-08-06  
17 <160> NUMBER OF SEQ ID NOS: 10  
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 1269  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Pyrococcus horikoshii  
26 <220> FEATURE:  
27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (1)...(1269)  
30 <400> SEQUENCE: 1

31	atg ccg ctg aaa ttc ccg gaa atg ttt ctc ttt ggt acc gca aca tca	48
32	Met Pro Leu Lys Phe Pro Glu Met Phe Leu Phe Gly Thr Ala Thr Ser	
33	1 5 10 15	
35	tcc cat cag ata gag gga aat aat aga tgg aat gat tgg tgg tac tat	96
36	Ser His Gln Ile Glu Gly Asn Asn Arg Trp Asn Asp Trp Trp Tyr Tyr	
37	20 25 30	
39	gag cag att gga aag ctc ccc tac aga tct ggt aag gct tgc aat cac	144
40	Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His	
41	35 40 45	
43	tgg gaa ctt tac agg gat gat att cag cta atg acc agc ttg ggc tat	192
44	Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr	
45	50 55 60	
47	aat gct tat agg ttc tcc ata gag tgg agc agg cta ttc cca gag gaa	240
48	Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu	
49	65 70 75 80	
51	aat aaa ttt aat gaa gat gct ttc atg aaa tac cgg gag att ata gac	288
52	Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp	
53	85 90 95	
55	ttg tta ttg acg aga ggt ata act ccc ctg gtg acc cta cac cac ttt	336
56	Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe	
57	100 105 110	
59	act agc cct ctc tgg ttc atg aag aaa ggt ggc ttc ctt agg gag gag	384
60	Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu	
61	115 120 125	
63	aac cta aaa cat tgg gaa aag tac ata gaa aag gtt gct gag ctt tta	432
64	Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu	
65	130 135 140	
67	gaa aaa gtt aaa cta gta gct acc ttc aat gag ccg atg gta tac gta	480

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68 Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val
69 145 150 155 160
71 atg atg gga tat cta acg gct tat tgg ccc cca ttc att agg agt cca 528
72 Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro
73 165 170 175
75 ttt aag gcc ttt aag gta gct gca aac ctg ctt aaa gct cac gca att 576
76 Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile
77 180 185 190
79 gcc tat gaa ctt ctt cat ggg aaa ttc aaa gtt gga atc gta aag aat 624
80 Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn
81 195 200 205
83 att ccc ata ata ctc cca gcg agt gac aag gag agg gat aga aaa gcc 672
84 Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala
85 210 215 220
87 gct gag aaa gct gat aat tta ttt aac tgg cac ttt ttg gat gcg ata 720
88 Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile
89 225 230 235 240
91 tgg agt ggg aaa tac aga ggg gta ttt aaa aca tat agg att ccc caa 768
92 Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln
93 245 250 255
95 agt gac gca gat ttc att ggg gtt aac tat tac acg gcc agc gaa gta 816
96 Ser Asp Ala Asp Phe Ile Gly Val Asn Tyr Tyr Thr Ala Ser Glu Val
97 260 265 270
99 agg cat act tgg aat cct tta aaa ttc ttt gag gtg aaa tta gcg 864
100 Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala
101 275 280 285
103 gat att agc gag agg aag act caa atg gga tgg agc gtt tat cca aaa 912
104 Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys
105 290 295 300
107 gga ata tac atg gcc ctt aaa aaa gct tcc agg tat gga agg cct ctt 960
108 Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Arg Tyr Gly Arg Pro Leu
109 305 310 315 320
111 tat att acg gaa aac gga ata gcg acg ctt gat gat gaa tgg aga gtg 1008
112 Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val
113 325 330 335
115 gaa ttc ata att caa cac ctc caa tac gtt cat aag gct atc gaa gac 1056
116 Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp
117 340 345 350
119 ggc ctg gat gta aga ggt tac ttc tat tgg tca ttt atg gat aac tac 1104
120 Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr
121 355 360 365
123 gag tgg aaa gag ggg ttt ggg cct aga ttt ggc cta gtg gaa gtt gat 1152
124 Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp
125 370 375 380
127 tat caa acc ttc gag aga agg ccc agg aag agt gct tac gta tac gga 1200
128 Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly
129 385 390 395 400
131 gaa att gca aga agt aag gaa ata aag gat gag cta tta aag aga tat 1248
132 Glu Ile Ala Arg Ser Lys Glu Ile Lys Asp Glu Leu Leu Lys Arg Tyr

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133          405          410          415          1269
135 ggc cta cca gaa ctt caa ctt
136 Gly Leu Pro Glu Leu Gln Leu
137          420
140 <210> SEQ ID NO: 2
141 <211> LENGTH: 423
142 <212> TYPE: PRT
143 <213> ORGANISM: Pyrococcus horikoshii
145 <400> SEQUENCE: 2
146 Met Pro Leu Lys Phe Pro Glu Met Phe Leu Phe Gly Thr Ala Thr Ser
147 1          5          10          15
148 Ser His Gln Ile Glu Gly Asn Asn Arg Trp Asn Asp Trp Trp Tyr Tyr
149          20          25          30
150 Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His
151          35          40          45
152 Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr
153          50          55          60
154 Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu
155 65          70          75          80
156 Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp
157          85          90          95
158 Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe
159          100         105         110
160 Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu
161          115         120         125
162 Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu
163          130         135         140
164 Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val
165 145         150         155         160
166 Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro
167          165         170         175
168 Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile
169          180         185         190
170 Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn
171          195         200         205
172 Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala
173          210         215         220
174 Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile
175 225         230         235         240
176 Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln
177          245         250         255
178 Ser Asp Ala Asp Phe Ile Gly Val Asn Tyr Tyr Thr Ala Ser Glu Val
179          260         265         270
180 Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala
181          275         280         285
182 Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys
183          290         295         300
184 Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Arg Tyr Gly Arg Pro Leu
185 305         310         315         320

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186 Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val
187           325           330           335
188 Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp
189           340           345           350
190 Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr
191           355           360           365
192 Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp
193           370           375           380
194 Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly
195 385           390           395           400
196 Glu Ile Ala Arg Ser Lys Glu Ile Lys Asp Glu Leu Leu Lys Arg Tyr
197           405           410           415
198 Gly Leu Pro Glu Leu Gln Leu
199           420
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 57
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: An upper primer designed to create the NdeI site.
209 <400> SEQUENCE: 3
210 taagaaggag atatacatat gccgctgaaa ttcccggaat tggttctctt tggtacc           57
212 <210> SEQ ID NO: 4
213 <211> LENGTH: 46
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: A lower primer designed to create the BamHI site.
220 <400> SEQUENCE: 4
221 ttactgcag agaggatccc taatcctaaa gttgaagttc tggtag           46
223 <210> SEQ ID NO: 5
224 <211> LENGTH: 423
225 <212> TYPE: PRT
226 <213> ORGANISM: Pyrococcus horikoshii
228 <400> SEQUENCE: 5
229 Met Pro Leu Lys Phe Pro Glu Met Phe Leu Phe Gly Thr Ala Thr Ser
230 1           5           10           15
231 Ser Lys Cys Ile Glu Gly Asn Asn Arg Trp Asn Cys Trp Trp Tyr Tyr
232           20           25           30
233 Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His
234           35           40           45
235 Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr
236           50           55           60
237 Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu
238 65           70           75           80
239 Asn Lys Phe Met Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp
240           85           90           95
241 Leu Leu Leu Thr Phe Gly Ile Thr Pro Leu Val Thr Leu His His Phe
242           100           105           110

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243 Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu
244      115      120      125
245 Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu
246      130      135      140
247 Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val
248 145      150      155      160
249 Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro
250      165      170      175
251 Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile
252      180      185      190
253 Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn
254      195      200      205
255 Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala
256      210      215      220
257 Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile
258 225      230      235      240
259 Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln
260      245      250      255
261 Ser Asp Ala Asp Phe Ile Gly Met Asn Tyr Tyr Thr Ala Ser Glu Val
262      260      265      270
263 Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala
264      275      280      285
265 Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys
266      290      295      300
267 Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Pro Tyr Gly Arg Pro Leu
268 305      310      315      320
269 Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val
270      325      330      335
271 Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp
272      340      345      350
273 Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr
274      355      360      365
275 Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp
276      370      375      380
277 Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly
278 385      390      395      400
279 Glu Ile Ala Arg Ser Lys Glu Ile Lys Asp Glu Leu Leu Lys Arg Tyr
280      405      410      415
281 Gly Leu Pro Glu Leu Gln Leu
282      420
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 483
286 <212> TYPE: PRT
287 <213> ORGANISM: Pyrococcus horikoshii
289 <400> SEQUENCE: 6
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291 1      5      10      15
292 Gly Asp Pro Tyr Arg Arg Asn Ile Asp Pro Arg Ser Asp Trp Trp Tyr
293      20      25      30

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VERIFICATION SUMMARY

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